

#5

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/511,538
Source: PCT/10
Date Processed by STIC: 10/27/04

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PCT

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/511,538

DATE: 10/27/2004

TIME: 10:51:43

Input Set : A:\sequence listing.txt

Output Set: N:\CRF4\10272004\J511538.raw

3 <110> APPLICANT: OriGene Technologies, Inc
 5 <120> TITLE OF INVENTION: TISSUE SPECIFIC GENES AND GENE CLUSTERS
 7 <130> FILE REFERENCE: 16U 200 PCT
 C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/511,538
 C--> 9 <141> CURRENT FILING DATE: 2004-10-18
 9 <150> PRIOR APPLICATION NUMBER: US 60/372,669
 10 <151> PRIOR FILING DATE: 2002-04-16
 12 <150> PRIOR APPLICATION NUMBER: US 60/411,882
 13 <151> PRIOR FILING DATE: 2002-09-20
 15 <150> PRIOR APPLICATION NUMBER: US 60/424,336
 16 <151> PRIOR FILING DATE: 2002-11-07
 18 <150> PRIOR APPLICATION NUMBER: US 60/374,823
 19 <151> PRIOR FILING DATE: 2002-04-24
 21 <150> PRIOR APPLICATION NUMBER: US 60/376,558
 22 <151> PRIOR FILING DATE: 2002-05-01
 24 <150> PRIOR APPLICATION NUMBER: US 60/381,366
 25 <151> PRIOR FILING DATE: 2002-05-20
 27 <150> PRIOR APPLICATION NUMBER: US 60/403,648
 28 <151> PRIOR FILING DATE: 2002-08-16
 30 <160> NUMBER OF SEQ ID NOS: 344
 32 <170> SOFTWARE: PatentIn version 3.1
 34 <210> SEQ ID NO: 1
 35 <211> LENGTH: 795
 36 <212> TYPE: DNA
 37 <213> ORGANISM: Homo sapiens
 39 <220> FEATURE:
 40 <221> NAME/KEY: CDS
 41 <222> LOCATION: (1)..(795)
 42 <223> OTHER INFORMATION:
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46 Met Glu Arg Val Asn Glu Thr Val Val Arg Glu Val Ile Phe Leu Gly	
47 1 5 10 15	
49 ttc tca tcc ctg gcc agg ctg cag cag ctg ctc ttt gtt atc ttc ctg	96
50 Phe Ser Ser Leu Ala Arg Leu Gln Gln Leu Leu Phe Val Ile Phe Leu	
51 20 25 30	
53 ctc ctc tac ctg ttc act ctg ggc acc aat gca atc atc att tcc acc	144
54 Leu Leu Tyr Leu Phe Thr Leu Gly Thr Asn Ala Ile Ile Ser Thr	
55 35 40 45	
57 att gtc ctg gac agg gcc ctt cat atc ccc atg tac ttc ttc ctt gcc	192
58 Ile Val Leu Asp Arg Ala Leu His Ile Pro Met Tyr Phe Phe Leu Ala	
59 50 55 60	
61 atc ctc tct tgc tct gag att tgc tac acc ttc atc att gta ccc aag	240

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63	65					70						75				80
65	atg	ctg	gtt	gac	ctg	ctg	tcc	cag	aag	aag	acc	att	tct	tcc	ctg	ggc
66	Met	Leu	Val	Asp	Leu	Leu	Ser	Gln	Lys	Lys	Thr	Ile	Ser	Phe	Leu	Gly
67								85				90				95
69	tgt	gcc	atc	caa	atg	ttt	tcc	tcc	tcc	ttt	ggc	tgc	tct	cac	tcc	
70	Cys	Ala	Ile	Gln	Met	Phe	Ser	Phe	Leu	Phe	Leu	Gly	Cys	Ser	His	Ser
71								100				105				110
73	ttt	ctg	ctg	gca	gtc	atg	ggt	tat	gat	cgt	tac	ata	gcc	atc	tgt	aac
74	Phe	Leu	Leu	Ala	Val	Met	Gly	Tyr	Asp	Arg	Tyr	Ile	Ala	Ile	Cys	Asn
75								115				120				125
77	cca	ctg	cgc	tac	tca	gtg	cta	atg	gga	cat	ggg	gtg	tgt	atg	gga	cta
78	Pro	Leu	Arg	Tyr	Ser	Val	Leu	Met	Gly	His	Gly	Val	Cys	Met	Gly	Leu
79								130				135				140
81	gtg	gct	gct	gcc	tgt	gcc	tgt	ggc	ttc	act	gtt	gca	cag	atc	atc	aca
82	Val	Ala	Ala	Ala	Cys	Ala	Cys	Gly	Phe	Thr	Val	Ala	Gln	Ile	Ile	Thr
83								145				150				160
85	tcc	ttg	gta	ttt	cac	ctg	cct	ttt	tat	tcc	tcc	aat	caa	cta	cat	cac
86	Ser	Leu	Val	Phe	His	Leu	Pro	Phe	Tyr	Ser	Ser	Asn	Gln	Leu	His	His
87								165				170				175
89	ttc	ttc	tgt	gac	att	gct	cct	gtc	ctc	aag	ctg	gca	tct	cac	cat	aac
90	Phe	Phe	Cys	Asp	Ile	Ala	Pro	Val	Leu	Lys	Leu	Ala	Ser	His	His	Asn
91								180				185				190
93	cac	ttt	agt	cag	att	gtc	atc	ttc	atg	ctc	tgt	aca	ttg	gtc	ctg	gct
94	His	Phe	Ser	Gln	Ile	Val	Ile	Phe	Met	Leu	Cys	Thr	Leu	Val	Leu	Ala
95								195				200				205
97	atc	ccc	tta	ttg	ttg	atc	ttg	gtg	tcc	tat	gtt	cac	atc	ctc	tct	gcc
98	Ile	Pro	Leu	Leu	Ile	Leu	Val	Ser	Tyr	Val	His	Ile	Leu	Ser	Ala	
99								210				215				220
101	ata	ctt	cag	ttt	cct	tcc	aca	ctg	gga	gtg	ata	gca	aaa	agg	aag	ttt
102	Ile	Leu	Gln	Phe	Pro	Ser	Thr	Leu	Gly	Val	Ile	Ala	Lys	Arg	Lys	Phe
103								225				230				240
105	cac	aat	agt	gat	gat	ttc	tca	cat	tat	aac	tct	ttt	caa	gat	cca	cct
106	His	Asn	Ser	Asp	Asp	Phe	Ser	His	Tyr	Asn	Ser	Phe	Gln	Asp	Pro	Pro
107								245				250				255
109	gtc	aat	aaa	agt	ctc	ctg	att	gat	taa							795
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116	<212>	TYPE:	PRT													
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122	1					5					10					15
125	Phe	Ser	Ser	Leu	Ala	Arg	Leu	Gln	Gln	Leu	Leu	Phe	Val	Ile	Phe	Leu
126								20				25				30
129	Leu	Leu	Tyr	Leu	Phe	Thr	Leu	Gly	Thr	Asn	Ala	Ile	Ile	Ser	Thr	
130								35				40				45

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133 Ile Val Leu Asp Arg Ala Leu His Ile Pro Met Tyr Phe Phe Leu Ala
134      50           55           60
137 Ile Leu Ser Cys Ser Glu Ile Cys Tyr Thr Phe Ile Ile Val Pro Lys
138 65          70           75           80
141 Met Leu Val Asp Leu Leu Ser Gln Lys Lys Thr Ile Ser Phe Leu Gly
142          85           90           95
145 Cys Ala Ile Gln Met Phe Ser Phe Leu Phe Leu Gly Cys Ser His Ser
146          100          105          110
149 Phe Leu Leu Ala Val Met Gly Tyr Asp Arg Tyr Ile Ala Ile Cys Asn
150          115          120          125
153 Pro Leu Arg Tyr Ser Val Leu Met Gly His Gly Val Cys Met Gly Leu
154          130          135          140
157 Val Ala Ala Ala Cys Ala Cys Gly Phe Thr Val Ala Gln Ile Ile Thr
158 145          150          155          160
161 Ser Leu Val Phe His Leu Pro Phe Tyr Ser Ser Asn Gln Leu His His
162          165          170          175
165 Phe Phe Cys Asp Ile Ala Pro Val Leu Lys Leu Ala Ser His His Asn
166          180          185          190
169 His Phe Ser Gln Ile Val Ile Phe Met Leu Cys Thr Leu Val Leu Ala
170          195          200          205
173 Ile Pro Leu Leu Leu Ile Leu Val Ser Tyr Val His Ile Leu Ser Ala
174          210          215          220
177 Ile Leu Gln Phe Pro Ser Thr Leu Gly Val Ile Ala Lys Arg Lys Phe
178 225          230          235          240
181 His Asn Ser Asp Asp Phe Ser His Tyr Asn Ser Phe Gln Asp Pro Pro
182          245          250          255
185 Val Asn Lys Ser Leu Leu Ile Asp
186          260
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191 <212> TYPE: DNA
192 <213> ORGANISM: Homo sapiens
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217 <211> LENGTH: 807
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Input Set : A:\sequence listing.txt
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 231 ttt cta ttc atc ctt tca ttt tct gag tcc tgc tac act ttt gtc atc 96
 232 Phe Leu Phe Ile Leu Ser Phe Ser Glu Ser Cys Tyr Thr Phe Val Ile
 233 20 25 30
 235 atc cct cag ctg ctg gtc cac ctg ctc tca gac acc aag acc atc tcc 144
 236 Ile Pro Gln Leu Leu Val His Leu Leu Ser Asp Thr Lys Thr Ile Ser
 237 35 40 45
 239 ttc atg gcc tgt gcc acc cag ctg ttc ttt ttc ctt ggc ttt gct tgc 192
 240 Phe Met Ala Cys Ala Thr Gln Leu Phe Phe Phe Leu Gly Phe Ala Cys
 241 50 55 60
 243 acc aac tgc ctc ctc att gct gtg atg gga tat gat cgc tat gta gca 240
 244 Thr Asn Cys Leu Leu Ile Ala Val Met Gly Tyr Asp Arg Tyr Val Ala
 245 65 70 75 80
 247 att tgt cac cct ctg agg tac aca ctc atc ata aac aaa agg ctg ggg 288
 248 Ile Cys His Pro Leu Arg Tyr Thr Leu Ile Ile Asn Lys Arg Leu Gly
 249 85 90 95
 251 ttg gag ttg att tct ctc tca gga gcc aca ggt ttc ttt att gct ttg 336
 252 Leu Glu Leu Ile Ser Leu Ser Gly Ala Thr Gly Phe Phe Ile Ala Leu
 253 100 105 110
 255 gtg gcc acc aac ctc att tgt gac atg cgt ttt tgt ggc ccc aac agg 384
 256 Val Ala Thr Asn Leu Ile Cys Asp Met Arg Phe Cys Gly Pro Asn Arg
 257 115 120 125
 259 gtt aac cac tat ttc tgt gac atg gca cct gtt atc aag tta gcc tgc 432
 260 Val Asn His Tyr Phe Cys Asp Met Ala Pro Val Ile Lys Leu Ala Cys
 261 130 135 140
 263 act gac acc cat gtg aaa gag ctg gct tta ttt agc ctc agc atc ctg 480
 264 Thr Asp Thr His Val Lys Glu Leu Ala Leu Phe Ser Leu Ser Ile Leu
 265 145 150 155 160
 267 gta att atg gtg cct ttt ctg tta att ctc ata tcc tat ggc ttc ata 528
 268 Val Ile Met Val Pro Phe Leu Leu Ile Leu Ser Tyr Gly Phe Ile
 269 165 170 175
 271 gtt aac acc atc ctg aag atc ccc tca gct gag ggc aag aag gcc ttt 576
 272 Val Asn Thr Ile Leu Lys Ile Pro Ser Ala Glu Gly Lys Lys Ala Phe
 273 180 185 190
 275 gtc acc tgt gcc tca cat ctc act gtg gtc ttt gtc cac tat ggc tgt 624
 276 Val Thr Cys Ala Ser His Leu Thr Val Val Phe Val His Tyr Gly Cys
 277 195 200 205
 279 gcc tct atc atc tat ctg cgg ccc aag tcc aag tct gct gcc tca gac aag 672
 280 Ala Ser Ile Ile Tyr Leu Arg Pro Lys Ser Lys Ser Ala Ser Asp Lys
 281 210 215 220
 283 gat cag ttg gtg gca gtg acc tac aca gtg gtt act ccc tta ctt aat 720

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Input Set : A:\sequence listing.txt
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284 Asp Gln Leu Val Ala Val Thr Tyr Thr Val Val Thr Pro Leu Leu Asn
 285 225 230 235 240
 287 cct ctt gtc tac agt ctg agg aac aaa gag gta aaa act gca ttg aaa 768
 288 Pro Leu Val Tyr Ser Leu Arg Asn Lys Glu Val Lys Thr Ala Leu Lys
 289 245 250 255
 291 aga gtt ctt gga atg cct gtg gca acc aag atg agc taa 807
 292 Arg Val Leu Gly Met Pro Val Ala Thr Lys Met Ser
 293 260 265
 296 <210> SEQ ID NO: 7
 297 <211> LENGTH: 268
 298 <212> TYPE: PRT
 299 <213> ORGANISM: Homo sapiens
 301 <400> SEQUENCE: 7
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 308 20 25 30
 311 Ile Pro Gln Leu Leu Val His Leu Leu Ser Asp Thr Lys Thr Ile Ser
 312 35 40 45
 315 Phe Met Ala Cys Ala Thr Gln Leu Phe Phe Leu Gly Phe Ala Cys
 316 50 55 60
 319 Thr Asn Cys Leu Leu Ile Ala Val Met Gly Tyr Asp Arg Tyr Val Ala
 320 65 70 75 80
 323 Ile Cys His Pro Leu Arg Tyr Thr Leu Ile Ile Asn Lys Arg Leu Gly
 324 85 90 95
 327 Leu Glu Leu Ile Ser Leu Ser Gly Ala Thr Gly Phe Phe Ile Ala Leu
 328 100 105 110
 331 Val Ala Thr Asn Leu Ile Cys Asp Met Arg Phe Cys Gly Pro Asn Arg
 332 115 120 125
 335 Val Asn His Tyr Phe Cys Asp Met Ala Pro Val Ile Lys Leu Ala Cys
 336 130 135 140
 339 Thr Asp Thr His Val Lys Glu Leu Ala Leu Phe Ser Leu Ser Ile Leu
 340 145 150 155 160
 343 Val Ile Met Val Pro Phe Leu Leu Ile Leu Ile Ser Tyr Gly Phe Ile
 344 165 170 175
 347 Val Asn Thr Ile Leu Lys Ile Pro Ser Ala Glu Gly Lys Lys Ala Phe
 348 180 185 190
 351 Val Thr Cys Ala Ser His Leu Thr Val Val Phe Val His Tyr Gly Cys
 352 195 200 205
 355 Ala Ser Ile Ile Tyr Leu Arg Pro Lys Ser Lys Ser Ala Ser Asp Lys
 356 210 215 220
 359 Asp Gln Leu Val Ala Val Thr Tyr Thr Val Val Thr Pro Leu Leu Asn
 360 225 230 235 240
 363 Pro Leu Val Tyr Ser Leu Arg Asn Lys Glu Val Lys Thr Ala Leu Lys
 364 245 250 255
 367 Arg Val Leu Gly Met Pro Val Ala Thr Lys Met Ser
 368 260 265
 371 <210> SEQ ID NO: 8
 372 <211> LENGTH: 25

VERIFICATION SUMMARY
PATENT APPLICATION: US/10/511,538

DATE: 10/27/2004
TIME: 10:51:44

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